

FIG. 1A

FIG. 1B

FIG. 1C

FIG. 1D

FIG. 1E

FIG. 1F

FIG. 1

1 GGATCCTGGT CGCGAGCGCG CGGCCAGCC ACCTGCCGGC GCGCCCCGCC

GGGACCGCTC GAGGACGCCT CGCGAAGGCT CTAGGGGCTG TATCTTCAAG

101 AGTCTACGCC CCTTTGTTGC AGTGCACAAA TTCCGTGCT AGCTTCATGC

"-35"

TATCAGGCC CAGACGAGGA AGATTCACCG ^{*phaE*} TGAACGATAC GGCCAACAAG
S/D V N D T A N K

201 ACCAGCGACT GGCTGGACAT CCAACGCAAG TACTGGGAGA CCTGGTCGGA
T S D W L D I Q R K Y W E T W S E

GCTCGGCCGC AAGACCTTGG GTCTGGAGAA GACCCCGGCC AATCCTTGGG
L G R E T L G L E K T P A N P W A

301 CCGGCGCCCT CGATCATTGG TGGCAGACGG TCTCGCCCGC CGCCCCAAC
G A L D H W W Q T V S P A A P N

GACTGGTTC GCGACTTCAT GGAGAAGCTC GCGAGCAGG GCAAGGCCTT
D T V R D T M E K I A T Q G K A E

401 CTTCGGGCTC ACCGACTACT TCACGAAGGG CCTCGGCGGC AGTAGCGGTA
F G L T D Y F T K G L G G S S G T

CGCAGGGCTG GGACACCCTC TCGAAGACCA TCGACGACAT GCAAAAGGCC

FIG. 1A

501 TTCGCCAGCG GCCGGATCGA AGGCGACGAG ACCTTCCGCC GCCTGATGGC
 F A S G R I E G D E T F R R L M A

 CTTCTGGGAG ATGCCGCTCG ACAACTGGCA GCGCACCATG TCCTCGCTGT
 F W E M P L D N W Q R T M S S L S

 601 CCCCAGGTGCC CGGCGACCTG CTGCGCAACA TGCCGCACGA CCAAGTCAGG
 P V P G D L L R N M P H D Q V R

 GACAGCGTCG ACCGCATCCT CTCGGCACCC GGGCTCGGCT ACACGCGCGA
 D S V D R I L S A P G I G Y T R E

 701 GGAGCAGGCC CGCTACCAGG ATCTGATCCG CCGCTCGCTG GAGTACCACT
 E Q A R Y Q D L I R R S L E Y Q S

 CGGCCCTGAA CGAATACAAC GGCTTCTTCG GCCAGCTCGG TGTCAAGTCC
 A L N E Y N G F F G Q L G V K S

 801 CTCGAGCGGA TGCGCGCCTT CCTGCAGGGA CAGGCCGAGA AGGGCGTCGC
 L E R M R A F L Q G Q A E K G V A

 CATCGAGTCG GCGCGCACCC TCTACGACGC CTGGGTCTGGC TGCTGCGAAG
 I F S A R T I Y D A W V G C C E E

 901 AGGTCTATGC CGAGGAGGTC AGCTCTGCG ACTACGCGCA CATCTACGTC
 V Y A E E V S S A D Y A H I H G

 CGCCTCGTCA ACGCCCAGAT GGCCCTCAAG CAGCGCATGT CGACCATGGT
 R I V N A Q M A I K Q R M S I M V

FIG. 1B

1001 CGACGAGGTC CTCGGCGCGA TGCCGCTGCC GACCCGCAGC GAGCTGCCCA
D E V L G A M P L P T R S E L R T

CGCTCCAGGA TCGGCTCCAG GAGTCGCCCG GCGAGGGCAA GCGCCAGCGC
L Q D R L Q E S R G E G K R Q R

1101 CAAGAGATCG AGACGCTGAA GCGGCAGGTC GCGGCCTTGG CCGGCGGGCG
Q F I E T L K R Q V A A L A G G A

CCAGCCCGCG CCCGAGGCCT CCGCCAGCC CAGCACCCGG CCGCGCGCGG
Q P A P Q A S A Q P S T R P A P A

1201 CGACGGCCCC GCGGGCGAGC GCGGGGCCCA AGCGCAGCAC CACGACCCGC
T A P A A S A A P K R S T T T R

CGCAAGACCA CCAAGCCCAC CACCGGCCAG TGATGTGGG CCCCCGTCCA
R E T T K P T T G Q *

1301 TCGCCACCAG *phaC*
GAGAGAGTGC $\xrightarrow{\quad}$ CGTGTCCCCA TTCCCGATCG ACATCCGGCC
S/D V S P F P I D I R P

CGACAAGCTG ACCGAGGAGA TGCTGGAGTA CAGCCGCAAG CTCGGCGAGG
D K I T T T M L T Y S R K L G G

1401 GTATGACGAA CCGCTCAAG GCGACACAGA TCGACACAGG CGTCACCCCG
M Q N L L F A D Q I D T G V T P

AAGGACGTGG TCCACCGCGA GGACAAGCTG GTCTCTACG GCTACCGGGG

1501 CCGGGCGCAG GTGGCGACCC AGAGGATCCC GCTGCTGATC GTCTACGCCC
P A Q V A T Q T I P L L I V Y A L

TCGTCAATCG GCCCTACATG ACCGACATCC AGGAGGATCG CTCGACGATC
V N R P Y M T D I Q E D R S T I

1601 AAGGGCCTGC TCGCCACCGG TCAGGACGTC TATCTGATCG ACTGGGGCTA
K G L L A T G Q D V Y L I D W G Y

CCCGGATCAG GCCGACCGGG CGCTGACCCT CGATGACTAC ATCAACGGCT
P D Q A D R A I T L D D Y I N G Y

1701 ACATCGACCG CTGCGTCGAC TACCTGCGCG AGACCCACGG CGTCGACCAG
I D R C V D Y L R E T H G V D Q

GTCAACCTGC TCGGGATCTG CCAGGGCGGG GCCTTCAGCC TCTGCTACAC
V N L L G I C Q G G A F S L C Y T

1801 GGCCCTGCAC TCCGAGAAGG TCAAAAACCT CGTCACCATG GTCACGCCGG
A L H S E K V K N L V T M V T P V

TCGACTTCCA GACCCCGGGC AACCTGCTCT CGGCCTGGGT CCAGAACGTC
D F Q T P G N I L S A W V Q N V

1901 GAGCTCGAC TGGCCGTCCA CACCATGGGC AACATCTGG GCGAATGCT
D V D L A V D I M G N I P G F I L

CAACTGGACC TTCCTGTCGC TCAAGCCCTT CAGCCTGACC GGCCAGAAGT
N W I F L S I K P F S I I G Q K Y

FIG. 1D

2001 ACGTCAACAT GGTCGACCTG CTCGACGACG AGGACAAGGT CAAGAACTTC
V N M V D L L D D E D K V K N F

CTGCGGATGG AGAAGTGGAT CTTCGACAGC CCGGACCAGG CCGGCGAGAC
L R M E K W I F D S P D Q A G E T

2101 CTTCCGCCAG TTCATCAAGG ACTTCTACCA GCGCAACGGC TTCATCAACG
F R Q F I K D F Y Q R N G F I N G

GCGGCGTCCT GATCGGGCGAT CAGGAGGTGG ACCTGCGCAA CATCCGCTGC
G V L I G D Q E V D L R N I R C

2201 CCGGTCCTGA ACATCTACCC GATGCAGGAC CACCTGGTGC CGCCGGATGC
P V L N I Y P M Q D H L V P P D A

CTCCAAGGCC CTGCGGGGAC TGACCTCCAG CGAGGACTAC ACGGAGCTCG
S K A L A G L T S S E D Y T E L A

2301 CCTTCCCCGG CGGGCACATC GGCATCTACG TCAGCGGCAA GGCGCAGGAA
F P G G H I G I Y V S G K A Q E

GGAGTCACCC CGGCGATCGG CCGCTGGCTG AACGAACGGG GCTGAGCCGG
G V T P A I G R W L N E R G *

2401 GTCGACCCAC CCGCTCGACG GCGCGGGCCG GCGGCATCGA AGCCCGCCGG

CGGGCGCCAA TGAGCATCC GCGCGGCTGG CGCCCGCCCC CCGACCTTCG

FIG. 1E

2501 CCGCCGCACC CGCATCGCCC CCGCGGGCTGG CGTACAATGA CGGTCTTCGC

GAGCGAGCCC CGCATCGTCA ACGGAGGCTG CATGGGCGCC GACCACCAAC

2601 TGCTGGCCGC GTACGACGGC CTGGCCGAGA CCTACGACGC CCACCGCGGC

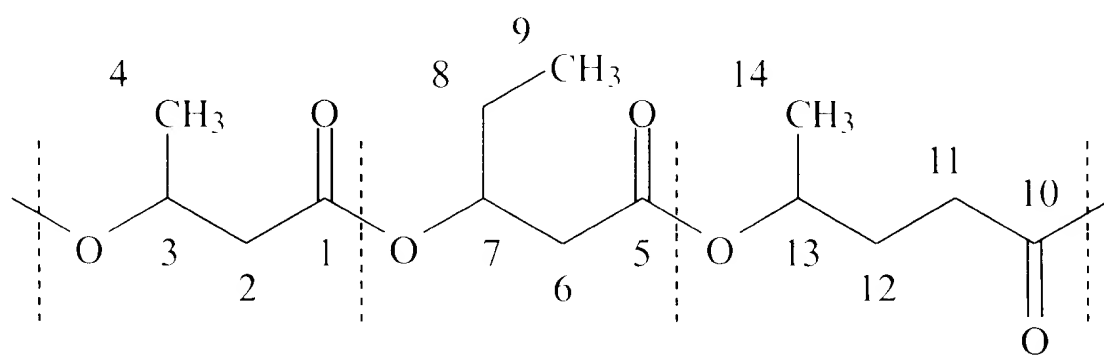
CTCTTCGACA TGGCGCCGT GCTCGAGGAC ATCTTCGCCC GCCTGCCGGC

2701 CTGCGGCACC CTCCTCGACC TCGGCTGCGG CGCCGGGGAG CCGTGCGCGC

GCGCCTTCCT CGACCGCGGC TGGCGGGTGA CCGGGGTGGA CTTCTGCCCG

2801 GCCATGCTCG CCCTCGCGGC GCGCTACGTC CCCGAGATGG AGCGGATCC

FIG. 1F



3HB

3HV

4HV

FIG. 2

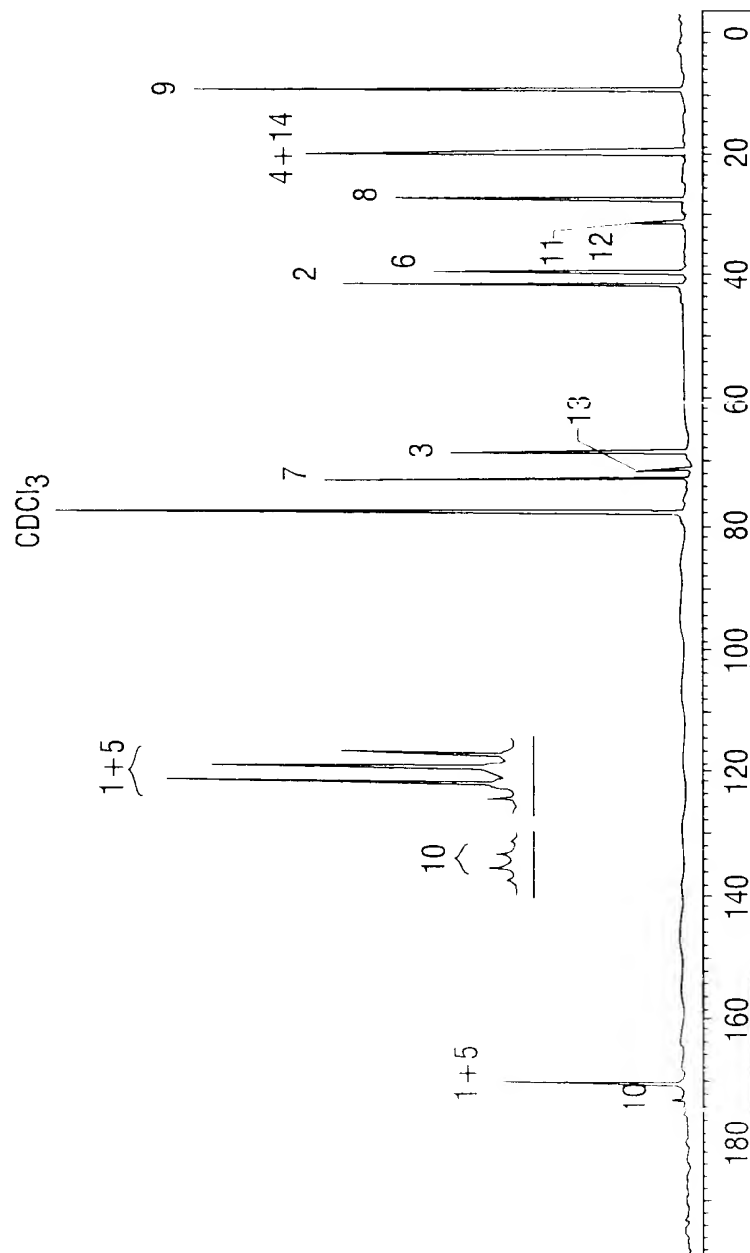


FIG. 3

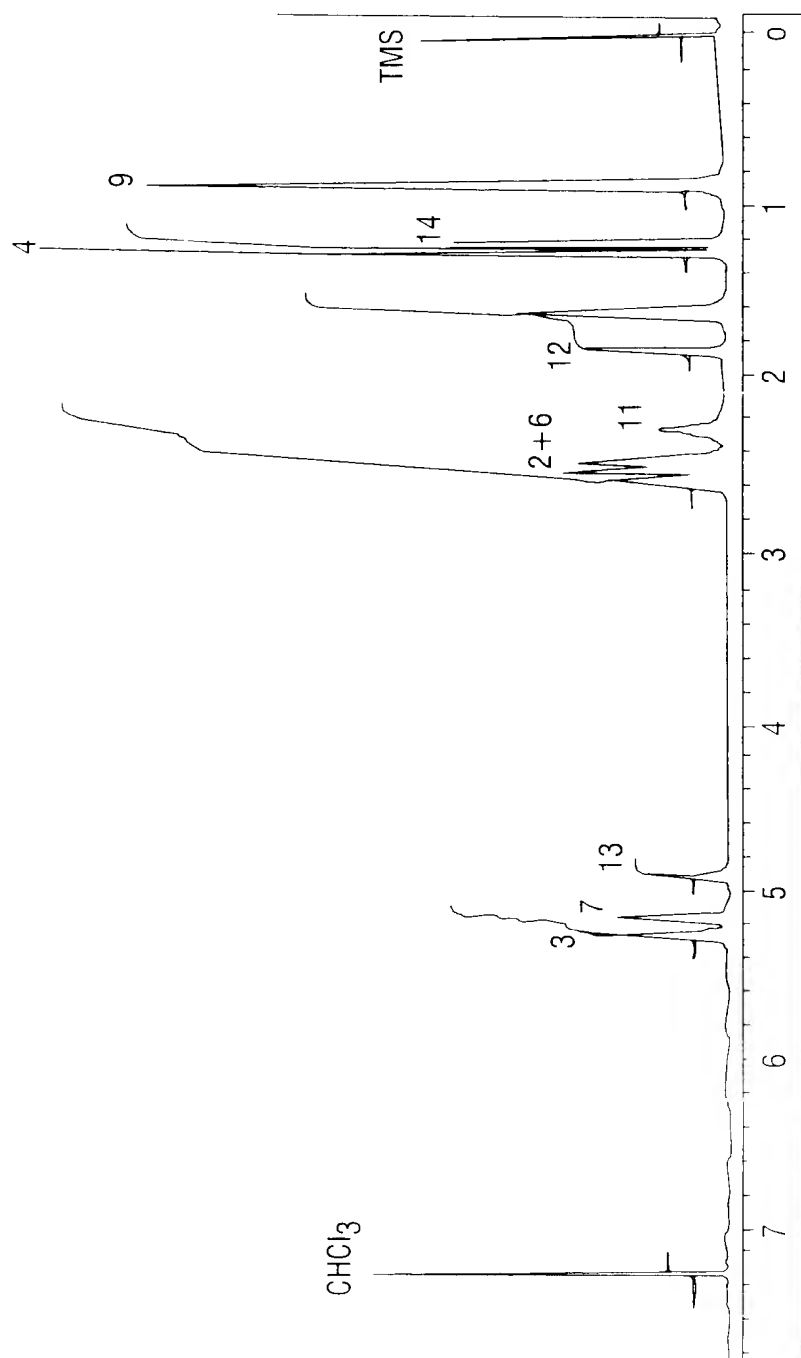


FIG. 4

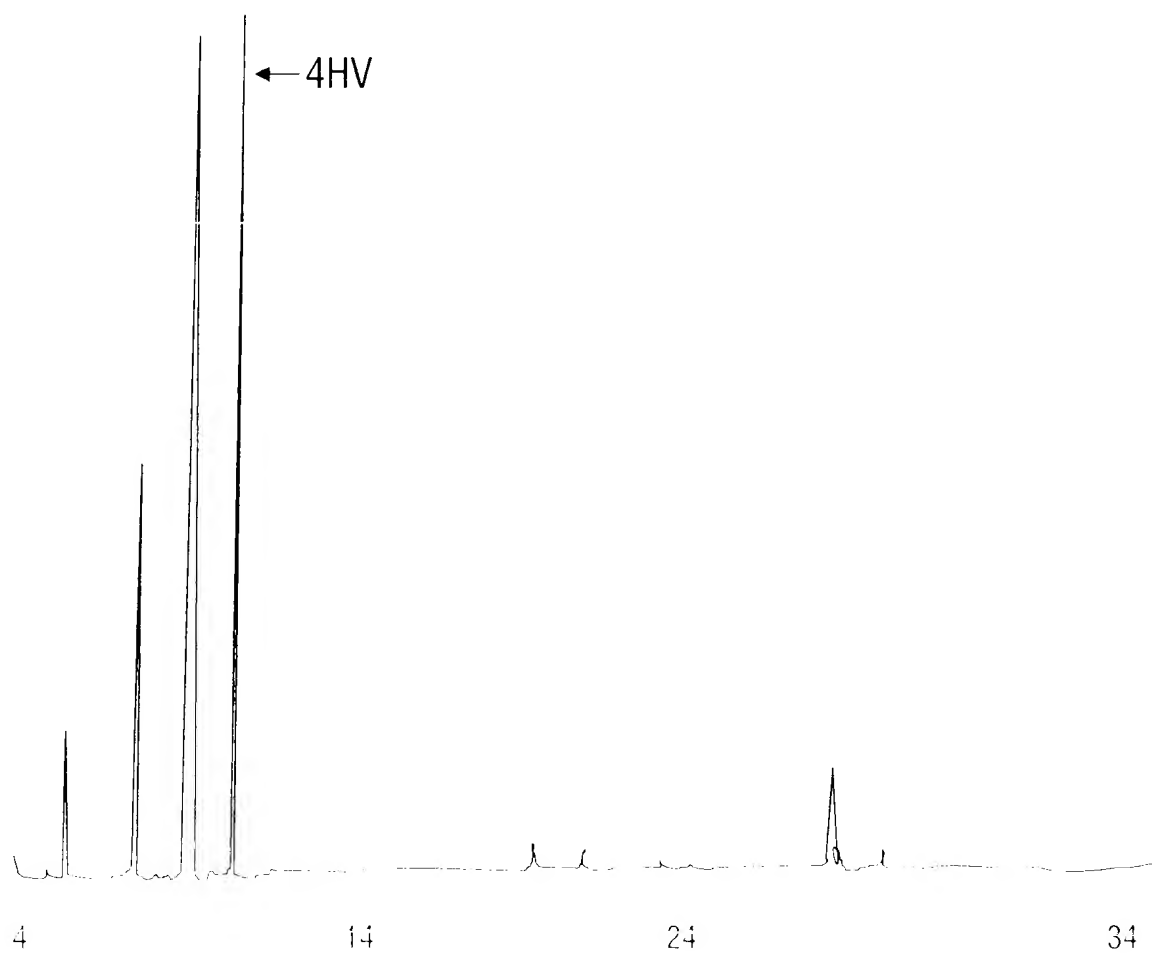


FIG. 5

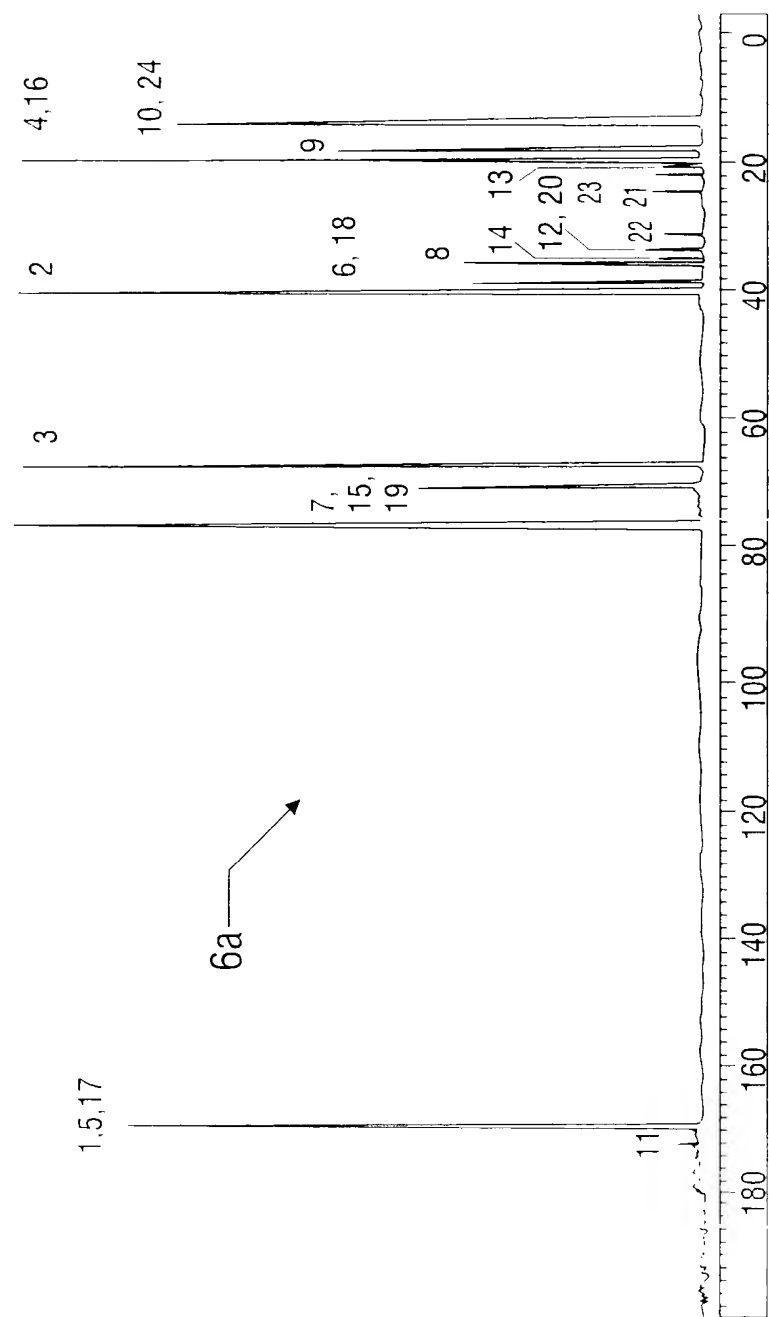


FIG. 6

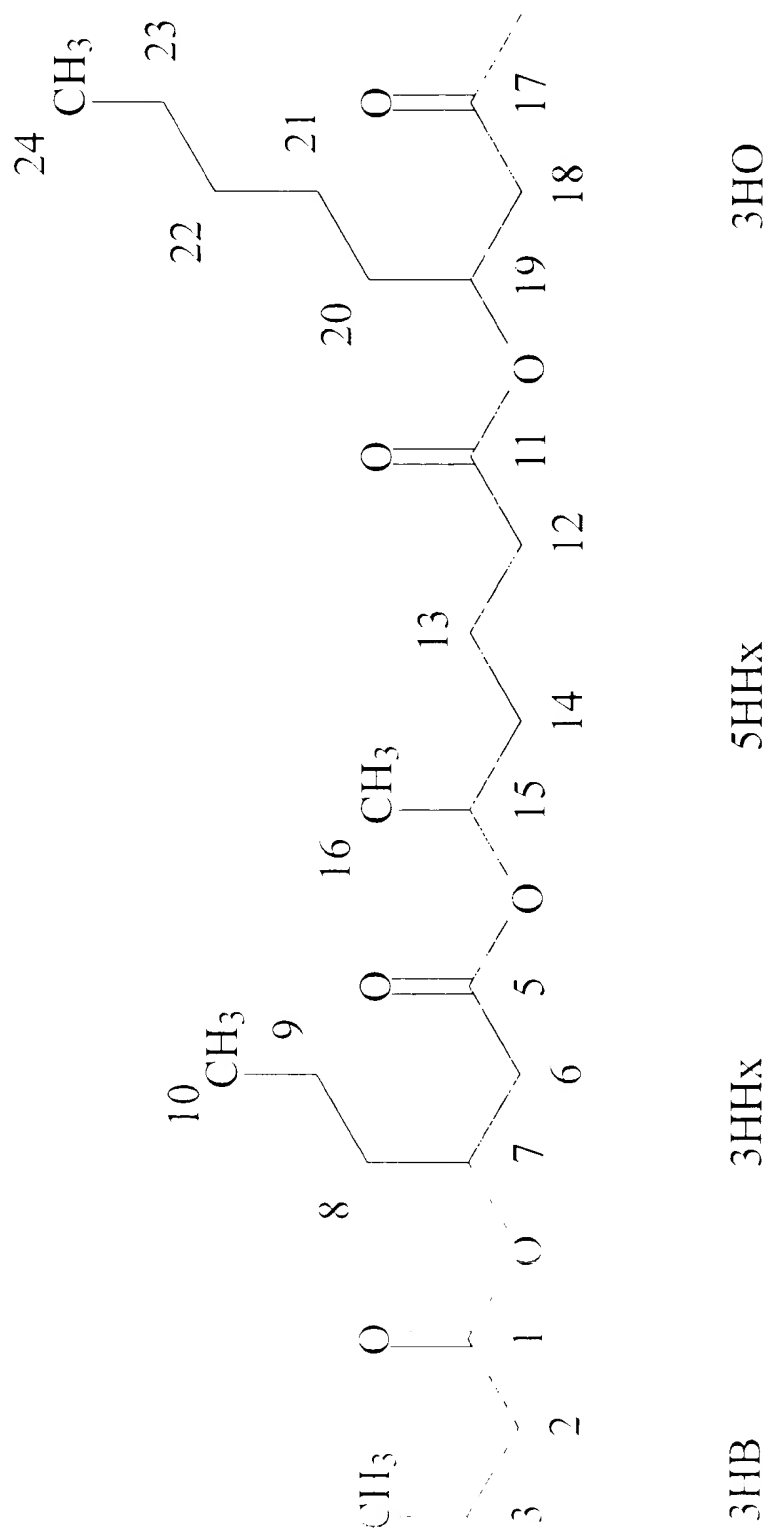


FIG. 6A

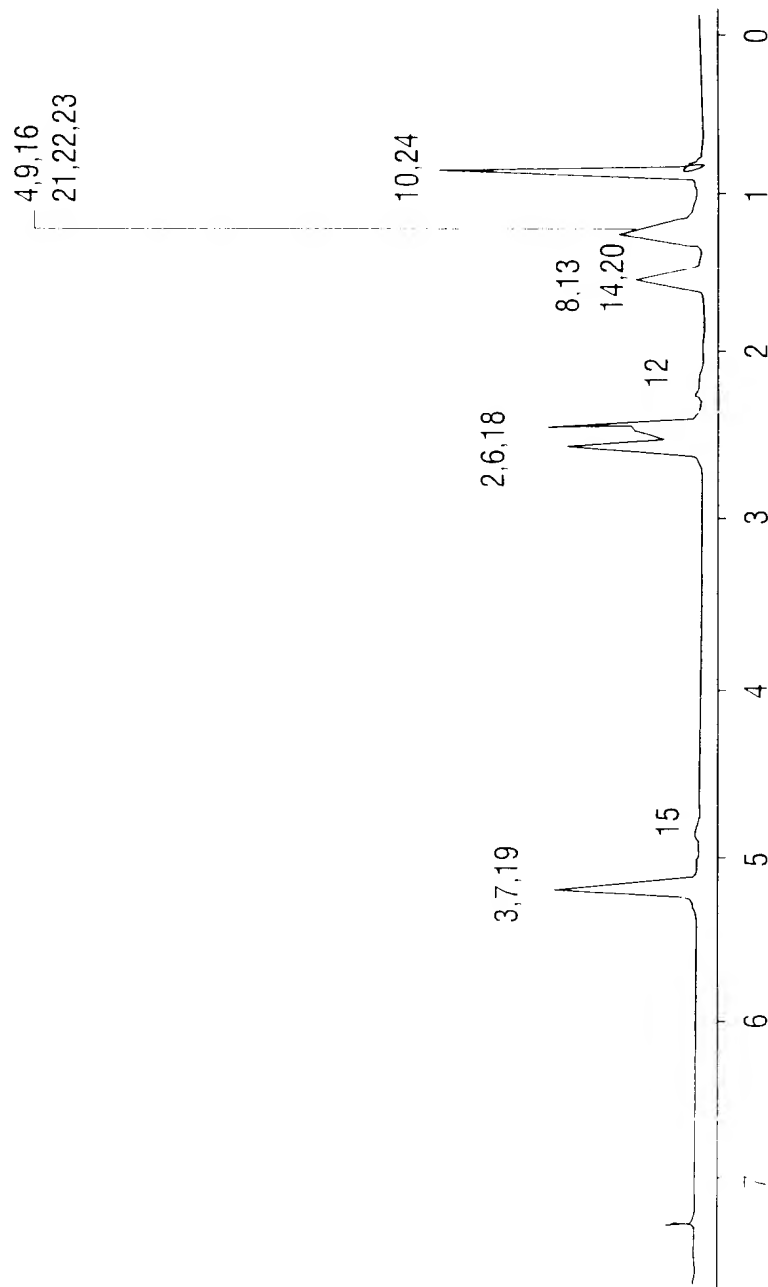


FIG. 7

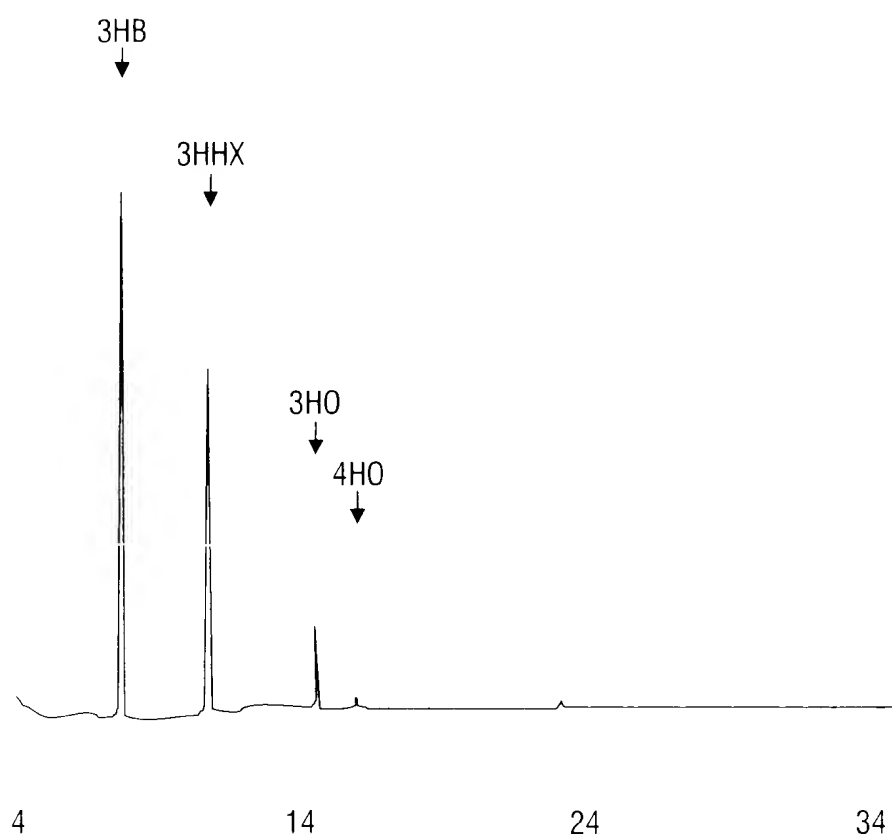


FIG. 8

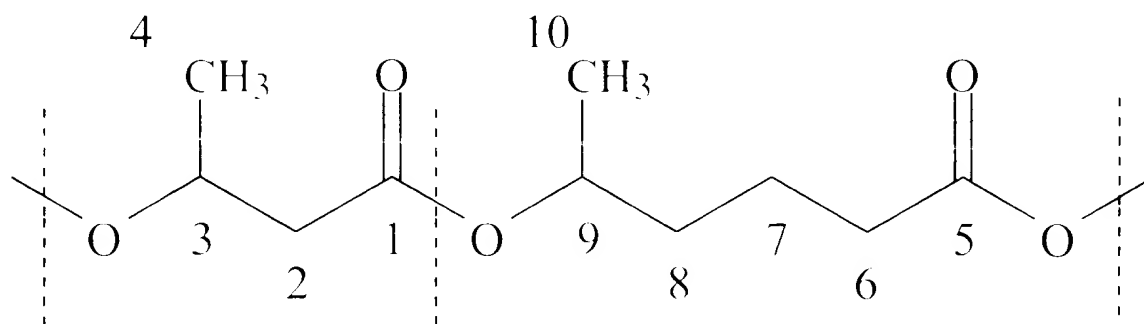


FIG. 9

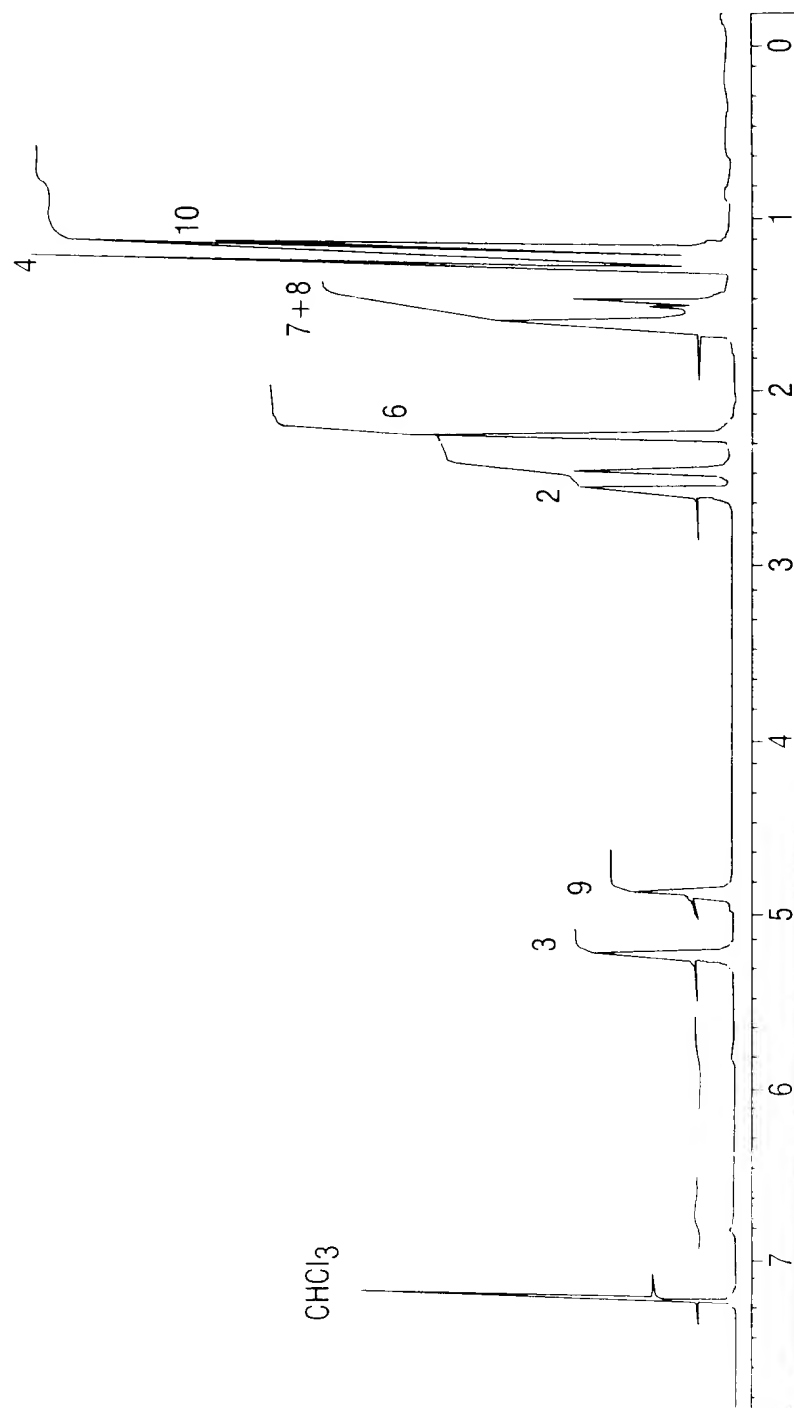


FIG. 10

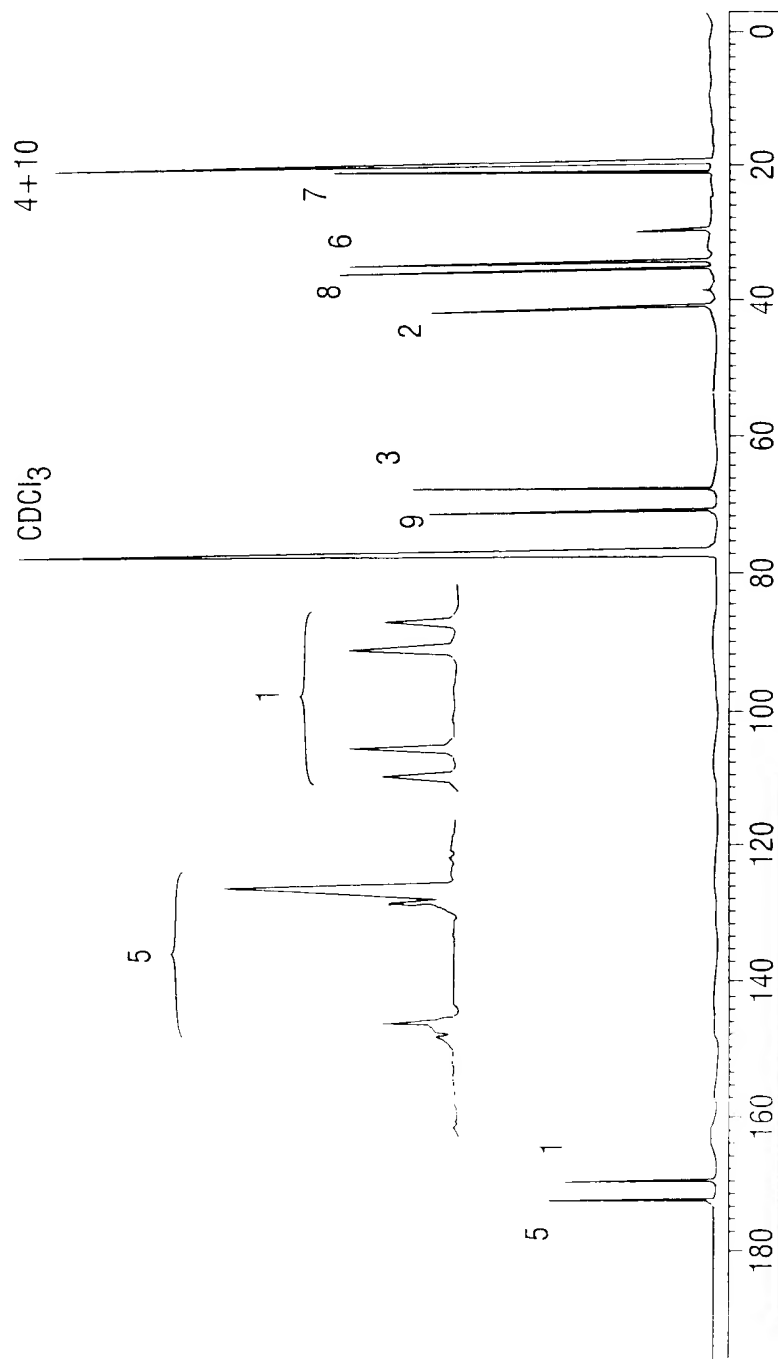


FIG. 11

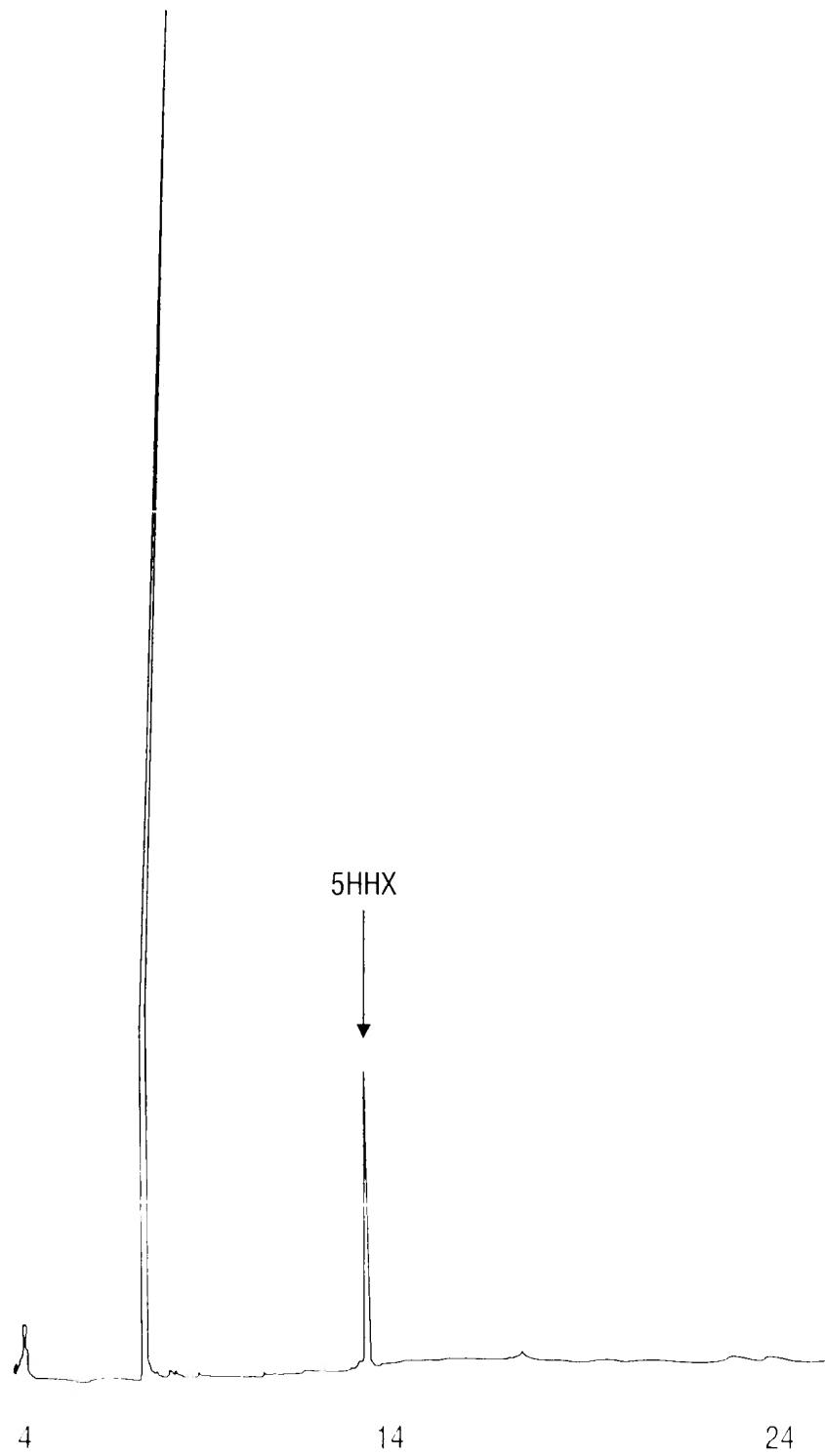


FIG. 12

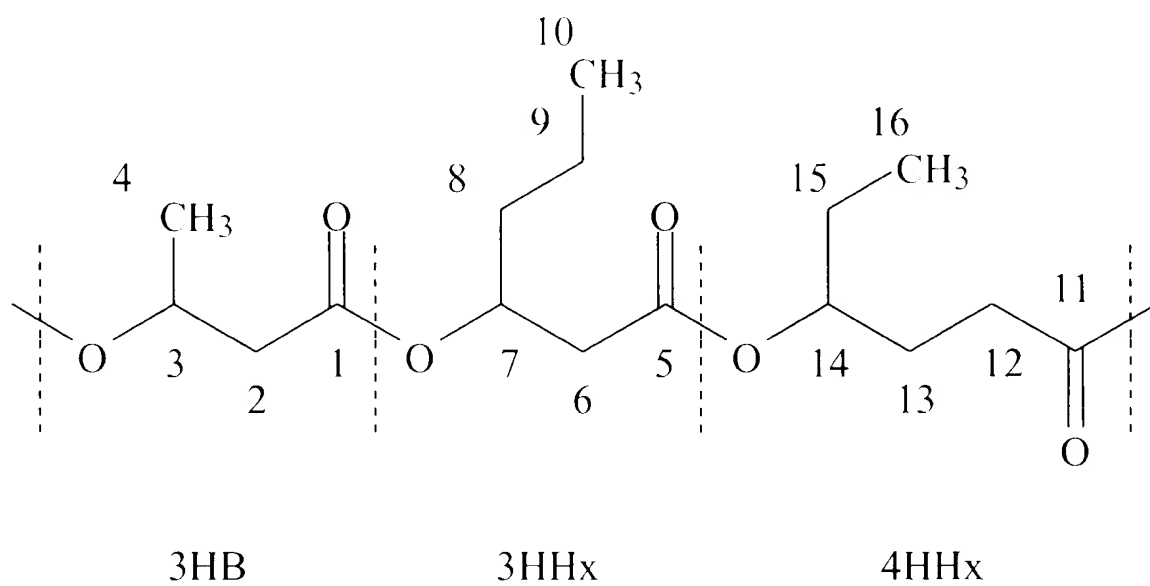


FIG. 13

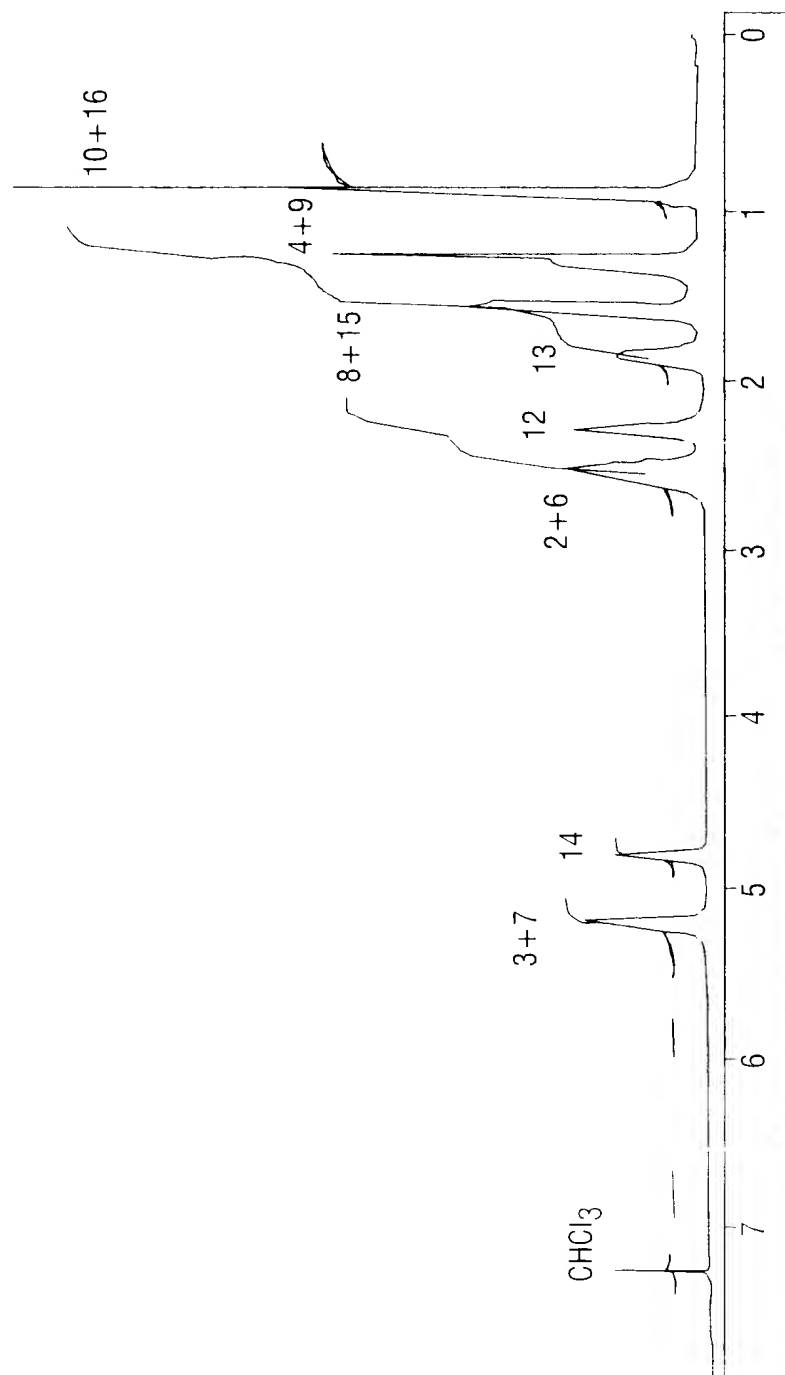


FIG. 14

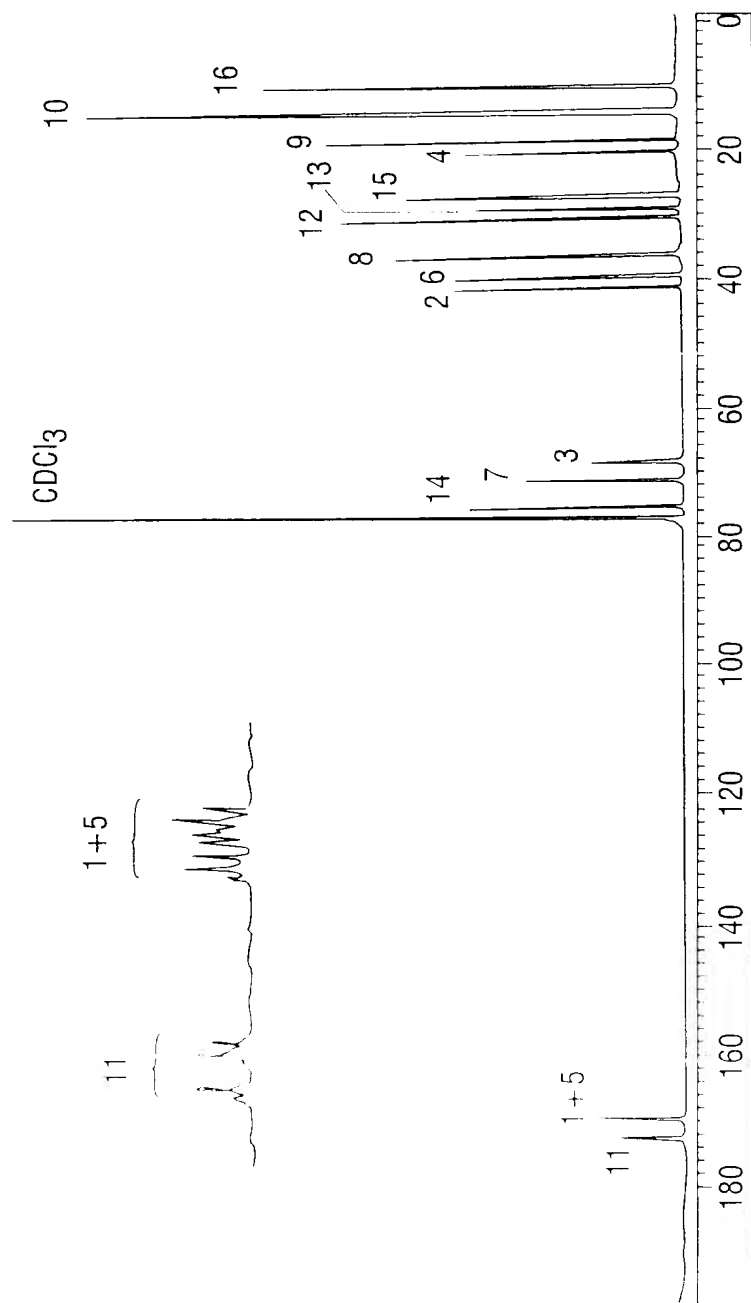


FIG. 15

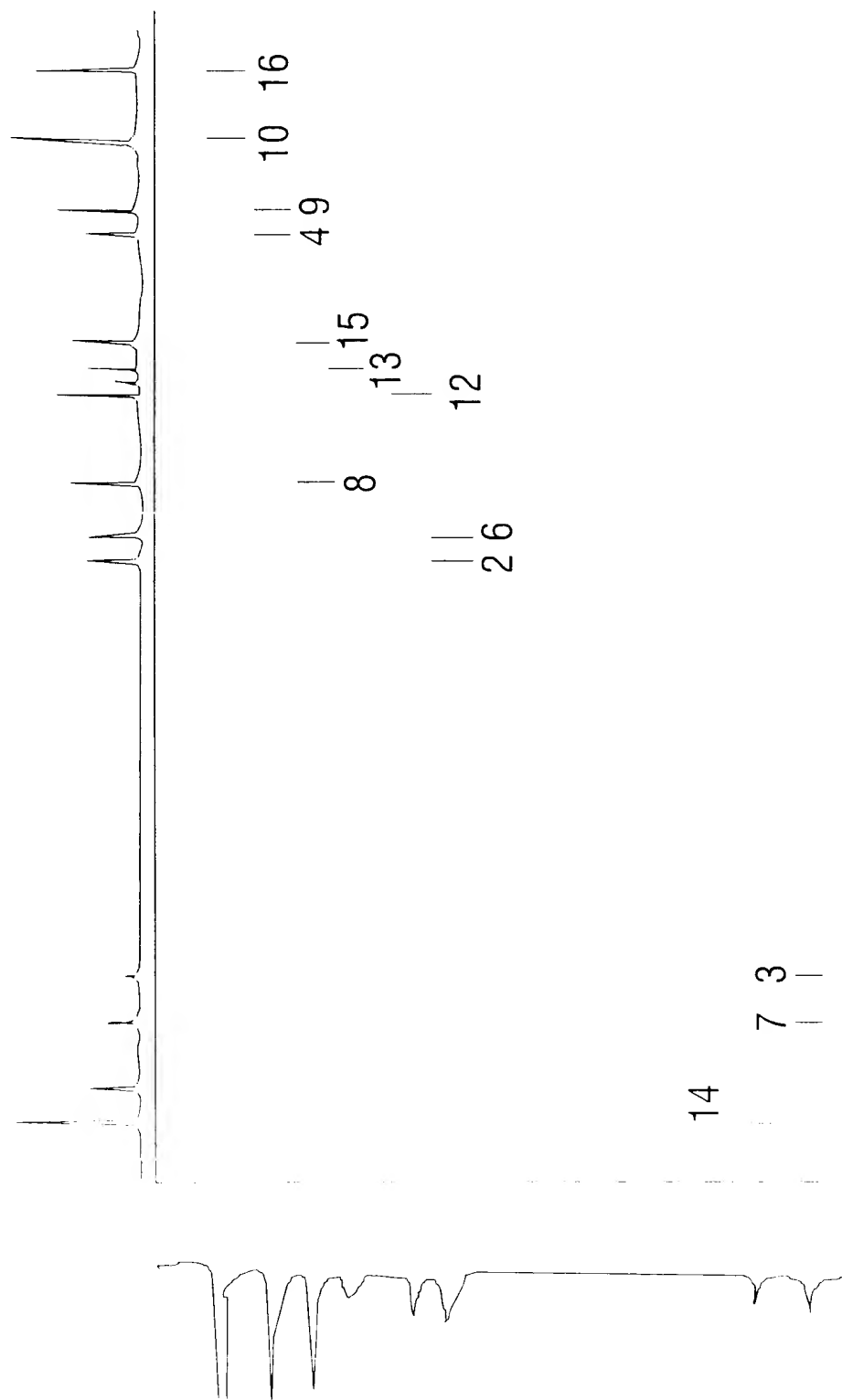


FIG. 16

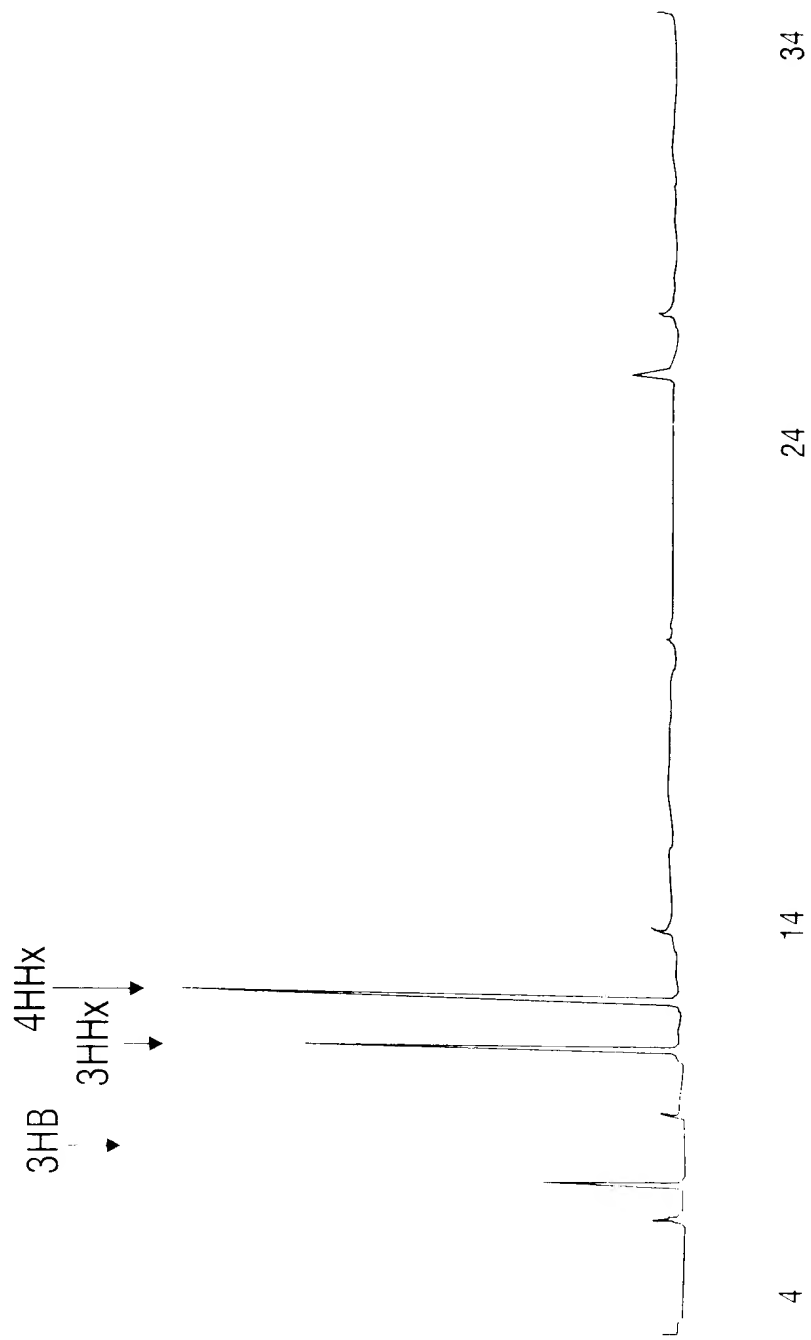


FIG. 17